

SEQUENCE LISTING

<110> Friddle, Carl Johan
Hilbun, Erin
Nepomnichy, Boris
Hu, Yi

<120> Novel Human Kinase Proteins and Polynucleotides Encoding the Same

<130> LEX-0227-USA

<150> US 60/229,280

<151> 2000-08-31

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2052

<212> DNA

<213> homo sapiens

<400> 1

atggataagt	acgatgtgat	taaggccatc	gggcaaggtg	ccttcgggaa	agcataactta	60
gctaaaggga	aatcagatag	caagcactgt	gtcataaaaag	agatcaattt	tgaaaagatg	120
cccatacaag	aaaaagaagc	ttcaaagaaa	gaagtgattc	ttctggaaaa	gatgaaacat	180
cccaacattg	tagccttctt	caattcattt	caagagaatg	gcaggctgtt	tattgtaatg	240
gaatattgtg	atggaggggga	tctcatgaaa	aggatcaata	gacaacgggg	tgtgttattt	300
agtgaagatc	agatcctcgg	ttggtttgta	cagatttctc	taggactaaa	acatattcat	360
gacaggaaga	tattacacag	ggacataaaa	gctcagaaca	tttttcttag	caagaacgga	420
atggtggcaa	agcttggggga	ctttggtata	gcaagagtcc	tgaataattc	catggaactt	480
gctcgaactt	gtattggaac	accttactac	ctgtccccag	agatctgtca	gaataaacc	540
tacaacaata	aaacggatat	ttggtctctt	ggctgtgtct	tatatgagct	ctgcacactt	600
aaacatcctt	ttgagggtaa	caacttacag	cagctgggtc	tgaagatttg	tcaagcacat	660
tttgccccaa	tatctccggg	gttttctcgt	gagctccatt	ccttgatata	tcagctcttt	720
caagtatctc	ctcgagaccg	accatccata	aattccattt	tgaaaaggcc	cttttttagag	780
aatcttattc	ccaaatatatt	gactcctgag	gtcattcagg	aagaattcag	tcacatgctt	840
atatgcagag	caggagcgcc	agcttctcga	catgctggga	aggtggtcca	gaagtgtaaa	900
atacaaaaag	tgagattcca	gggaaagtgc	ccaccaagat	caaggatata	tgtgccaat	960
aaaaggaatg	ctatatattga	tagaaatgaa	tggagaccac	cagctggagc	ccagaaggcc	1020
agatctataa	aaatgataga	aagacccaaa	attgctgctg	tctgtggaca	ttatgattat	1080
tattatgctc	aacttgatat	gctgaggagg	agagcccaca	aaccaagtta	tcaccctatt	1140
cctcaagaaa	atactggagt	tgaggattac	ggtcaggaaa	cgaggcatgg	tccatcccca	1200
agtcaatggc	ctgctgagta	ccttcagaga	aaatttgaag	ctcaacaata	taagttgaaa	1260
gtggagaagc	aattgggtct	tcgtccatct	tctgccgagc	caaattacaa	ccagagacaa	1320
gagctaagaa	gtaatggaga	agagcctaga	ttccaggagc	tgccatttag	gaaaaacgaa	1380
atgaaggaac	aggaatattg	gaagcagtta	gaggaaatac	gccaacagta	ccacaatgac	1440
atgaaagaaa	ttagaaagaa	gatggggaga	gaaccagagg	agaactcaaa	aataagtcac	1500
aaaacctatt	tgggtgaagaa	gagtaacctg	cctgtccatc	aagatgcatc	tgaggggagaa	1560
gcacctgtgc	aggacattga	aaaagacttg	aaacaaatga	ggcttcagaa	cacaaaggaa	1620
agtaaaaaatc	cagaacagaa	atataaaagct	aagaaggggg	taaaatttga	aattaattta	1680
gacaaatgta	tttctgatga	aaacatcctc	caagaggaag	aggcaatgga	tataccaaat	1740
gaaactttga	cctttgagga	tggcatgaag	tttaaggaat	atgaatgtgt	aaaggagcat	1800
ggagattata	cagacaaaagc	atttgaaaaa	cttcactgcc	cagaagcagg	gttttccacg	1860

cagactgtag	ctgctgtggg	aaacaggagg	cagtgggatg	gaggagcgcc	tcagactctg	1920
ctgcagatga	tggcagtggc	cgacatcacc	tccacctgcc	ccacggggcc	tgacagtgag	1980
tctgtgctta	gcgtcagtcg	tcaggaaggg	aagaccaagg	accgtacag	cccagtgtc	2040
atcctgatgt	ga					2052

<210> 2
 <211> 683
 <212> PRT
 <213> homo sapiens

<400> 2

Met	Asp	Lys	Tyr	Asp	Val	Ile	Lys	Ala	Ile	Gly	Gln	Gly	Ala	Phe	Gly	
1				5					10					15		
Lys	Ala	Tyr	Leu	Ala	Lys	Gly	Lys	Ser	Asp	Ser	Lys	His	Cys	Val	Ile	
			20					25					30			
Lys	Glu	Ile	Asn	Phe	Glu	Lys	Met	Pro	Ile	Gln	Glu	Lys	Glu	Ala	Ser	
			35				40						45			
Lys	Lys	Glu	Val	Ile	Leu	Leu	Glu	Lys	Met	Lys	His	Pro	Asn	Ile	Val	
			50				55				60					
Ala	Phe	Phe	Asn	Ser	Phe	Gln	Glu	Asn	Gly	Arg	Leu	Phe	Ile	Val	Met	
65					70					75					80	
Glu	Tyr	Cys	Asp	Gly	Gly	Asp	Leu	Met	Lys	Arg	Ile	Asn	Arg	Gln	Arg	
				85					90					95		
Gly	Val	Leu	Phe	Ser	Glu	Asp	Gln	Ile	Leu	Gly	Trp	Phe	Val	Gln	Ile	
			100					105					110			
Ser	Leu	Gly	Leu	Lys	His	Ile	His	Asp	Arg	Lys	Ile	Leu	His	Arg	Asp	
			115				120					125				
Ile	Lys	Ala	Gln	Asn	Ile	Phe	Leu	Ser	Lys	Asn	Gly	Met	Val	Ala	Lys	
			130				135					140				
Leu	Gly	Asp	Phe	Gly	Ile	Ala	Arg	Val	Leu	Asn	Asn	Ser	Met	Glu	Leu	
145					150					155					160	
Ala	Arg	Thr	Cys	Ile	Gly	Thr	Pro	Tyr	Tyr	Leu	Ser	Pro	Glu	Ile	Cys	
				165					170					175		
Gln	Asn	Lys	Pro	Tyr	Asn	Asn	Lys	Thr	Asp	Ile	Trp	Ser	Leu	Gly	Cys	
			180					185					190			
Val	Leu	Tyr	Glu	Leu	Cys	Thr	Leu	Lys	His	Pro	Phe	Glu	Gly	Asn	Asn	
			195				200					205				
Leu	Gln	Gln	Leu	Val	Leu	Lys	Ile	Cys	Gln	Ala	His	Phe	Ala	Pro	Ile	
			210			215					220					
Ser	Pro	Gly	Phe	Ser	Arg	Glu	Leu	His	Ser	Leu	Ile	Ser	Gln	Leu	Phe	
225					230					235					240	
Gln	Val	Ser	Pro	Arg	Asp	Arg	Pro	Ser	Ile	Asn	Ser	Ile	Leu	Lys	Arg	
				245					250					255		
Pro	Phe	Leu	Glu	Asn	Leu	Ile	Pro	Lys	Tyr	Leu	Thr	Pro	Glu	Val	Ile	
			260					265					270			
Gln	Glu	Glu	Phe	Ser	His	Met	Leu	Ile	Cys	Arg	Ala	Gly	Ala	Pro	Ala	
			275				280					285				
Ser	Arg	His	Ala	Gly	Lys	Val	Val	Gln	Lys	Cys	Lys	Ile	Gln	Lys	Val	
			290			295					300					
Arg	Phe	Gln	Gly	Lys	Cys	Pro	Pro	Arg	Ser	Arg	Ile	Ser	Val	Pro	Ile	
305					310					315					320	
Lys	Arg	Asn	Ala	Ile	Leu	His	Arg	Asn	Glu	Trp	Arg	Pro	Pro	Ala	Gly	
				325					330					335		
Ala	Gln	Lys	Ala	Arg	Ser	Ile	Lys	Met	Ile	Glu	Arg	Pro	Lys	Ile	Ala	
			340					345					350			
Ala	Val	Cys	Gly	His	Tyr	Asp	Tyr	Tyr	Tyr	Ala	Gln	Leu	Asp	Met	Leu	

355	360	365
Arg Arg Arg Ala His Lys Pro Ser Tyr His Pro Ile Pro Gln Glu Asn		
370	375	380
Thr Gly Val Glu Asp Tyr Gly Gln Glu Thr Arg His Gly Pro Ser Pro		
385	390	400
Ser Gln Trp Pro Ala Glu Tyr Leu Gln Arg Lys Phe Glu Ala Gln Gln		
405	410	415
Tyr Lys Leu Lys Val Glu Lys Gln Leu Gly Leu Arg Pro Ser Ser Ala		
420	425	430
Glu Pro Asn Tyr Asn Gln Arg Gln Glu Leu Arg Ser Asn Gly Glu Glu		
435	440	445
Pro Arg Phe Gln Glu Leu Pro Phe Arg Lys Asn Glu Met Lys Glu Gln		
450	455	460
Glu Tyr Trp Lys Gln Leu Glu Glu Ile Arg Gln Gln Tyr His Asn Asp		
465	470	475
Met Lys Glu Ile Arg Lys Lys Met Gly Arg Glu Pro Glu Glu Asn Ser		
485	490	495
Lys Ile Ser His Lys Thr Tyr Leu Val Lys Lys Ser Asn Leu Pro Val		
500	505	510
His Gln Asp Ala Ser Glu Gly Glu Ala Pro Val Gln Asp Ile Glu Lys		
515	520	525
Asp Leu Lys Gln Met Arg Leu Gln Asn Thr Lys Glu Ser Lys Asn Pro		
530	535	540
Glu Gln Lys Tyr Lys Ala Lys Lys Gly Val Lys Phe Glu Ile Asn Leu		
545	550	555
Asp Lys Cys Ile Ser Asp Glu Asn Ile Leu Gln Glu Glu Glu Ala Met		
565	570	575
Asp Ile Pro Asn Glu Thr Leu Thr Phe Glu Asp Gly Met Lys Phe Lys		
580	585	590
Glu Tyr Glu Cys Val Lys Glu His Gly Asp Tyr Thr Asp Lys Ala Phe		
595	600	605
Glu Lys Leu His Cys Pro Glu Ala Gly Phe Ser Thr Gln Thr Val Ala		
610	615	620
Ala Val Gly Asn Arg Arg Gln Trp Asp Gly Gly Ala Pro Gln Thr Leu		
625	630	635
Leu Gln Met Met Ala Val Ala Asp Ile Thr Ser Thr Cys Pro Thr Gly		
645	650	655
Pro Asp Ser Glu Ser Val Leu Ser Val Ser Arg Gln Glu Gly Lys Thr		
660	665	670
Lys Asp Pro Tyr Ser Pro Val Leu Ile Leu Met		
675	680	

<210> 3

<211> 1965

<212> DNA

<213> homo sapiens

<400> 3

atggataagt acgatgtgat taaggccatc gggcaagggtg ccttcgggaa agcataactta	60
gctaaaggga aatcagatag caagcactgt gtcataaaaag agatcaattt tgaaaagatg	120
cccatacaag aaaaagaagc ttcaaagaaa gaagtgattc ttctggaaaa gatgaaacat	180
ccaacattg tagccttctt caattcattt caagagaatg gcaggctgtt tattgtaatg	240
gaatattgtg atggagggga tctcatgaaa aggatcaata gacaacgggg tgtgttattt	300
agtgaagatc agatcctcgg ttggtttgta cagatttctc taggactaaa acatattcat	360
gacaggaaga tattacacag ggacataaaa gctcagaaca tttttcttag caagaacgga	420
atggtggcaa agcttgggga ctttggtata gcaagagtcc tgaataattc catggaactt	480

gctcgaactt	gtattggaac	accttactac	ctgtccccag	agatctgtca	gaataaaccc	540
tacaacaata	aaacggatat	ttggtctctt	ggctgtgtct	tatatgagct	ctgcacactt	600
aaacatcctt	ttgagggtaa	caacttacag	cagctgggtc	tgaagatttg	tcaagcacat	660
tttgcccca	tatctccggg	gttttctcgt	gagctccatt	ccttgatata	tcagctcttt	720
caagtatctc	ctcgagaccg	accatccata	aattccattt	tgaaaaggcc	cttttttagag	780
aatcttattc	ccaaatattt	gactcctgag	gtcattcagg	aagaattcag	tcacatgctt	840
atatgcagag	caggagcgcc	agcttctcga	catgctggga	aggtgggtcca	gaagtgtaaa	900
atacaaaaag	tgagattcca	gggaaagtgc	ccaccaagat	caaggatatc	tgtgccaatt	960
aaaaggaatg	ctatatgtga	tagaaatgaa	tggagaccac	cagctggagc	ccagaaggcc	1020
agatctataa	aaatgataga	aagacccaaa	attgctgctg	tctgtggaca	ttatgattat	1080
tattatgctc	aacttgatat	gctgaggagg	agagcccaca	aaccaagtta	tcacctatt	1140
cctcaagaaa	atactggagt	tgaggattac	ggtcaggaaa	cgaggcatgg	tccatcccca	1200
agtcaatggc	ctgctgagta	ccttcagaga	aaatttgaag	ctcaacaata	taagttgaaa	1260
gtggagaagc	aattgggtct	tcgtccatct	tctgccgagc	caaattacaa	ccagagacaa	1320
gagctaagaa	gtaatggaga	agagcctaga	ttccaggagc	tgccatttag	gaaaaacgaa	1380
atgaaggaac	aggagaactc	aaaaataagt	cataaaacct	atttggtgaa	gaagagtaac	1440
ctgcctgtcc	atcaagatgc	atctgaggga	gaagcacctg	tgccaggacat	tgaaaaagac	1500
ttgaaacaaa	tgaggcttca	gaacacaaa	gaaagtaaaa	atccagaaca	gaaatataaa	1560
gctaagaagg	gggtaaaatt	tgaaattaat	ttagacaaat	gtatttctga	tgaaaacatc	1620
ctccaagagg	aagaggcaat	ggatatacca	aatgaaactt	tgacctttga	ggatggcatg	1680
aagtttaagg	aatatgaatg	tgtaaaggag	catggagatt	atacagacaa	agcatttgaa	1740
aaacttcact	gcccagaagc	agggttttcc	acgcagactg	tagctgctgt	gggaaacagg	1800
aggcagtggg	atggaggagc	gcctcagact	ctgctgcaga	tgatggcagt	ggccgacatc	1860
acctccacct	gccccacggg	gcctgacagt	gagtcgtgtc	ttagcgtcag	tcgtcaggaa	1920
gggaagacca	aggaccgta	cagcccagtg	ctcatcctga	tgtga		1965

<210> 4

<211> 654

<212> PRT

<213> homo sapiens

<400> 4

Met	Asp	Lys	Tyr	Asp	Val	Ile	Lys	Ala	Ile	Gly	Gln	Gly	Ala	Phe	Gly
1				5				10						15	
Lys	Ala	Tyr	Leu	Ala	Lys	Gly	Lys	Ser	Asp	Ser	Lys	His	Cys	Val	Ile
			20					25					30		
Lys	Glu	Ile	Asn	Phe	Glu	Lys	Met	Pro	Ile	Gln	Glu	Lys	Glu	Ala	Ser
		35					40						45		
Lys	Lys	Glu	Val	Ile	Leu	Leu	Glu	Lys	Met	Lys	His	Pro	Asn	Ile	Val
	50					55					60				
Ala	Phe	Phe	Asn	Ser	Phe	Gln	Glu	Asn	Gly	Arg	Leu	Phe	Ile	Val	Met
65					70					75					80
Glu	Tyr	Cys	Asp	Gly	Gly	Asp	Leu	Met	Lys	Arg	Ile	Asn	Arg	Gln	Arg
				85					90					95	
Gly	Val	Leu	Phe	Ser	Glu	Asp	Gln	Ile	Leu	Gly	Trp	Phe	Val	Gln	Ile
				100					105					110	
Ser	Leu	Gly	Leu	Lys	His	Ile	His	Asp	Arg	Lys	Ile	Leu	His	Arg	Asp
		115						120					125		
Ile	Lys	Ala	Gln	Asn	Ile	Phe	Leu	Ser	Lys	Asn	Gly	Met	Val	Ala	Lys
		130					135					140			
Leu	Gly	Asp	Phe	Gly	Ile	Ala	Arg	Val	Leu	Asn	Asn	Ser	Met	Glu	Leu
145					150					155					160
Ala	Arg	Thr	Cys	Ile	Gly	Thr	Pro	Tyr	Tyr	Leu	Ser	Pro	Glu	Ile	Cys
				165					170					175	
Gln	Asn	Lys	Pro	Tyr	Asn	Asn	Lys	Thr	Asp	Ile	Trp	Ser	Leu	Gly	Cys
			180					185						190	

Val	Leu	Tyr	Glu	Leu	Cys	Thr	Leu	Lys	His	Pro	Phe	Glu	Gly	Asn	Asn
	195						200					205			
Leu	Gln	Gln	Leu	Val	Leu	Lys	Ile	Cys	Gln	Ala	His	Phe	Ala	Pro	Ile
	210					215				220					
Ser	Pro	Gly	Phe	Ser	Arg	Glu	Leu	His	Ser	Leu	Ile	Ser	Gln	Leu	Phe
225					230					235					240
Gln	Val	Ser	Pro	Arg	Asp	Arg	Pro	Ser	Ile	Asn	Ser	Ile	Leu	Lys	Arg
				245					250					255	
Pro	Phe	Leu	Glu	Asn	Leu	Ile	Pro	Lys	Tyr	Leu	Thr	Pro	Glu	Val	Ile
			260					265					270		
Gln	Glu	Glu	Phe	Ser	His	Met	Leu	Ile	Cys	Arg	Ala	Gly	Ala	Pro	Ala
		275					280					285			
Ser	Arg	His	Ala	Gly	Lys	Val	Val	Gln	Lys	Cys	Lys	Ile	Gln	Lys	Val
	290					295				300					
Arg	Phe	Gln	Gly	Lys	Cys	Pro	Pro	Arg	Ser	Arg	Ile	Ser	Val	Pro	Ile
305					310					315					320
Lys	Arg	Asn	Ala	Ile	Leu	His	Arg	Asn	Glu	Trp	Arg	Pro	Pro	Ala	Gly
				325					330					335	
Ala	Gln	Lys	Ala	Arg	Ser	Ile	Lys	Met	Ile	Glu	Arg	Pro	Lys	Ile	Ala
			340					345					350		
Ala	Val	Cys	Gly	His	Tyr	Asp	Tyr	Tyr	Tyr	Ala	Gln	Leu	Asp	Met	Leu
	355						360					365			
Arg	Arg	Arg	Ala	His	Lys	Pro	Ser	Tyr	His	Pro	Ile	Pro	Gln	Glu	Asn
	370					375					380				
Thr	Gly	Val	Glu	Asp	Tyr	Gly	Gln	Glu	Thr	Arg	His	Gly	Pro	Ser	Pro
385					390					395					400
Ser	Gln	Trp	Pro	Ala	Glu	Tyr	Leu	Gln	Arg	Lys	Phe	Glu	Ala	Gln	Gln
				405					410					415	
Tyr	Lys	Leu	Lys	Val	Glu	Lys	Gln	Leu	Gly	Leu	Arg	Pro	Ser	Ser	Ala
			420					425					430		
Glu	Pro	Asn	Tyr	Asn	Gln	Arg	Gln	Glu	Leu	Arg	Ser	Asn	Gly	Glu	Glu
		435					440					445			
Pro	Arg	Phe	Gln	Glu	Leu	Pro	Phe	Arg	Lys	Asn	Glu	Met	Lys	Glu	Gln
	450					455					460				
Glu	Asn	Ser	Lys	Ile	Ser	His	Lys	Thr	Tyr	Leu	Val	Lys	Lys	Ser	Asn
465					470					475					480
Leu	Pro	Val	His	Gln	Asp	Ala	Ser	Glu	Gly	Glu	Ala	Pro	Val	Gln	Asp
				485					490					495	
Ile	Glu	Lys	Asp	Leu	Lys	Gln	Met	Arg	Leu	Gln	Asn	Thr	Lys	Glu	Ser
			500					505					510		
Lys	Asn	Pro	Glu	Gln	Lys	Tyr	Lys	Ala	Lys	Lys	Gly	Val	Lys	Phe	Glu
		515					520					525			
Ile	Asn	Leu	Asp	Lys	Cys	Ile	Ser	Asp	Glu	Asn	Ile	Leu	Gln	Glu	Glu
	530					535					540				
Glu	Ala	Met	Asp	Ile	Pro	Asn	Glu	Thr	Leu	Thr	Phe	Glu	Asp	Gly	Met
545					550					555					560
Lys	Phe	Lys	Glu	Tyr	Glu	Cys	Val	Lys	Glu	His	Gly	Asp	Tyr	Thr	Asp
				565					570					575	
Lys	Ala	Phe	Glu	Lys	Leu	His	Cys	Pro	Glu	Ala	Gly	Phe	Ser	Thr	Gln
				580				585					590		
Thr	Val	Ala	Ala	Val	Gly	Asn	Arg	Arg	Gln	Trp	Asp	Gly	Gly	Ala	Pro
	595					600						605			
Gln	Thr	Leu	Leu	Gln	Met	Met	Ala	Val	Ala	Asp	Ile	Thr	Ser	Thr	Cys
	610				615						620				
Pro	Thr	Gly	Pro	Asp	Ser	Glu	Ser	Val	Leu	Ser	Val	Ser	Arg	Gln	Glu
625					630					635					640

Gly Lys Thr Lys Asp Pro Tyr Ser Pro Val Leu Ile Leu Met
645 650

<210> 5
<211> 2240
<212> DNA
<213> homo sapiens

<400> 5
ctgtctcatt tcagttatct gtggccacaa ggaaagttat ttgtctctgt cttggcaagg 60
ctgggaggaa agtttttagct aagaacctca gccattgga gaccatggat aagtacgatg 120
tgattaaggc catcgggcaa ggtgccttcg ggaaagcata cttagctaaa gggaaatcag 180
atagcaagca ctgtgtcata aaagagatca attttgaaaa gatgccata caagaaaaag 240
aagcttcaaa gaaagaagtg attcttctgg aaaagatgaa acatcccaac attgtagcct 300
tcttcaattc atttcaagag aatggcaggc tgtttattgt aatggaatat tgtgatggag 360
gggatctcat gaaaaggatc aatagacaac ggggtgtgtt atttagtgaa gatcagatcc 420
tcggttggtt tgtacagatt tctctaggac taaaacatat tcatgacagg aagatattac 480
acagggacat aaaagctcag aacatttttc ttagcaagaa cggaatggtg gcaaagcttg 540
gggacttttg tatagcaaga gtcctgaata attccatgga acttgctcga acttgtattg 600
gaacacctta ctacctgtcc ccagagatct gtcagaataa accctacaac aataaaacgg 660
atatttggtc tcttggtgtg gtccttatatg agctctgcac acttaaacad ccttttgagg 720
gtaacaactt acagcagctg gttctgaaga tttgtcaagc acattttgcc ccaatatctc 780
cggggttttc tcgtgagctc cattccttga tatctcagct ctttcaagta tctcctcgag 840
accgaccatc cataaattcc attttgaaaa ggcccttttt agagaatctt attcccaaatt 900
atttgactcc tgaggtcatt caggaagaat tcagtcacat gcttatatgc agagcaggag 960
cgccagcttc tcgacatgct gggaaggtgg tccagaagtg taaaatacaa aaagtggagat 1020
tccagggaaa gtgcccacca agatcaagga tatctgtgcc aattaaaagg aatgctatat 1080
tgcatagaaa tgaatggaga ccaccagctg gagcccagaa ggccagatct ataaaaatga 1140
tagaaaagacc caaaattgct gctgtctgtg gacattatga ttattattat gctcaacttg 1200
atatgctgag gaggagagcc cacaaaacaa gttatcacc ttttctcaa gaaaatactg 1260
gagttgagga ttacggtcag gaaacgaggc atggtccatc cccaagtcaa tggcctgctg 1320
agtaccttca gagaaaattt gaagctcaac aatataagtt gaaagtggag aagcaattgg 1380
gtcttctgct atcttctgcc gagccaaatt acaaccagag acaagagcta agaagtaatg 1440
gagaagagcc tagattccag gagctgcat ttaggaaaaa cgaaatgaag gaacaggaat 1500
attggaagca gttagaggaa atacgccaac agtaccacaa tgacatgaaa gaaattagaa 1560
agaagatggg gagagaacca gaggagaact caaaaataag tcataaaacc tatttggtga 1620
agaagagtaa cctgcctgtc catcaagatg catctgaggg agaagcacct gtgcaggaca 1680
ttgaaaaaga cttgaaacaa atgaggcttc agaacacaaa ggaaagtaaa aatccagaac 1740
agaaatataa agctaagaag ggggtaaaaat ttgaaattaa tttagacaaa tgtatttctg 1800
atgaaaacat cctccaagag gaagaggcaa tggatatacc aaatgaaact ttgacctttg 1860
aggatggcat gaagttaag gaatatgaat gtgtaaagga gcatggagat tatacagaca 1920
aagcatttga aaaacttcac tgcccagaag cagggttttc cacgcagact gtagctgctg 1980
tgggaaacag gaggcagtgg gatggaggag cgccctcagac tctgctgcag atgatggcag 2040
tgcccgacat caccctccacc tgccccacgg ggccctgacag tgagtctgtg cttagcgtca 2100
gtcgtcagga agggaaagacc aaggacccgt acagcccagt gctcatcctg atgtgatagt 2160
ctacttctca ctatacacc tatagatctt gtatcagaca ctttcaaata tgttgttttg 2220
atatctccct ataccaaaaa 2240

<210> 6
<211> 1167
<212> DNA
<213> homo sapiens

<400> 6
atgttaaaaag tgaagaggct ggaagaattc aacacgtgtt ataacagcaa ccagctggag 60
aaaatggcct tttttcagtg cagggaagag gtggagaaa tgaagtgttt tctggaaaaa 120

```

aattctgggg accaggattc aagatctgga cataatgagg cgaaggaggt gtggtcaaac 180
gccgacctga cggaaaggat gcccgtcaaa agcaaaagga catcagccct cgcagttgac 240
atccccgctc ctccggcccc atttgatcat cgtattgtga cagccaagca aggagcggtc 300
aacagcttct atactgtgag caagacagaa atcctaggag gagggcggtt cggccagggt 360
cacaagtgtg aggagacggc cacaggctctg aagctggcag ccaaaatcat caagaccaga 420
ggcatgaagg acaaggagga ggtgaagaac gagatcagcg tcatgaacca gctggaccac 480
gcgaacctca tccagctgta cgatgccttc gagtctaaga acgacattgt cctgggtcatg 540
gagtatgtgg atggtgggga gctgtttgac cgcatcatcg atgagagcta caatttgacg 600
gagcttgata ccattcctgtt catgaagcag atatgtgagg ggataaggca catgcatcag 660
atgtacattc tccacttgga cctgaagcct gagaatatcc tgtgtgtgaa tcgggatgct 720
aagcaaataa aaattattga ttttggattg gccagaagat acaaaccag agagaagctg 780
aaggtgaact ttggaacccc agaatttctc gcccctgaag ttgtgaacta tgattttgtt 840
tcatttccca ctgacatgtg gagtgtgggg gtcatcgctt atatgctact tagcggtttg 900
tcgcctttcc tgggtgacaa tgatgctgag acgctgaaca acatcctggc ctgcagggtg 960
gacttagagg atgaagaatt tcaggacatc tcggaggagg ccaaggagtt catctctaag 1020
cttctgatta aggagaagag ttggcgaata agtgcaagcg aagctctcaa gcacccttg 1080
ttgtcagacc acaagctcca ctccagactc aatgcccaga agaagaagaa tcgtggctct 1140
gatgccagg actttgtgac caaatag 1167

```

<210> 7

<211> 388

<212> PRT

<213> homo sapiens

<400> 7

```

Met Leu Lys Val Lys Arg Leu Glu Glu Phe Asn Thr Cys Tyr Asn Ser
 1          5          10          15
Asn Gln Leu Glu Lys Met Ala Phe Phe Gln Cys Arg Glu Glu Val Glu
          20          25          30
Lys Val Lys Cys Phe Leu Glu Lys Asn Ser Gly Asp Gln Asp Ser Arg
          35          40          45
Ser Gly His Asn Glu Ala Lys Glu Val Trp Ser Asn Ala Asp Leu Thr
          50          55          60
Glu Arg Met Pro Val Lys Ser Lys Arg Thr Ser Ala Leu Ala Val Asp
65          70          75          80
Ile Pro Ala Pro Pro Ala Pro Phe Asp His Arg Ile Val Thr Ala Lys
          85          90          95
Gln Gly Ala Val Asn Ser Phe Tyr Thr Val Ser Lys Thr Glu Ile Leu
          100          105          110
Gly Gly Gly Arg Phe Gly Gln Val His Lys Cys Glu Glu Thr Ala Thr
          115          120          125
Gly Leu Lys Leu Ala Ala Lys Ile Ile Lys Thr Arg Gly Met Lys Asp
          130          135          140
Lys Glu Glu Val Lys Asn Glu Ile Ser Val Met Asn Gln Leu Asp His
145          150          155          160
Ala Asn Leu Ile Gln Leu Tyr Asp Ala Phe Glu Ser Lys Asn Asp Ile
          165          170          175
Val Leu Val Met Glu Tyr Val Asp Gly Gly Glu Leu Phe Asp Arg Ile
          180          185          190
Ile Asp Glu Ser Tyr Asn Leu Thr Glu Leu Asp Thr Ile Leu Phe Met
          195          200          205
Lys Gln Ile Cys Glu Gly Ile Arg His Met His Gln Met Tyr Ile Leu
          210          215          220
His Leu Asp Leu Lys Pro Glu Asn Ile Leu Cys Val Asn Arg Asp Ala
225          230          235          240
Lys Gln Ile Lys Ile Ile Asp Phe Gly Leu Ala Arg Arg Tyr Lys Pro

```


tgctctagac	ttggagtggc	tcaagctctt	cgatgtgac	ctatcaatgt	caagagaaag	180
aagcactgaa	gagtcataat	tgtgtcctga	tttataaatc	ggagacagag	ggagacgaaa	240
accacactcc	agaaagtagc	ttaatcggac	tcactactaa	gatgttaaaa	gtgaagaggc	300
tggaagaatt	caacacgtgt	tataacagca	accagctgga	gaaaatggcc	ttttttcagt	360
gcagggaaga	ggtggagaaa	gtgaagtgtt	ttctggaaaa	aaatttctggg	gaccaggatt	420
caagatctgg	acataatgag	gcgaaggagg	tgtggtcaaa	cgccgacctg	acggaaagga	480
tgcccgtcaa	aagcaaaaagg	acatcagccc	tcgcagttga	catcccggct	cctccggccc	540
catttgatca	tcgtattgtg	acagccaagc	aaggagcggg	caacagcttc	tatactgtga	600
gcaagacaga	aatcctagga	ggagggcggt	tcggccagggt	tcacaagtgt	gaggagacgg	660
ccacaggtct	gaagctggca	gccaaaaatca	tcaagaccag	aggcatgaag	gacaaggagg	720
aggtgaagaa	cgagatcagc	gtcatgaacc	agctggacca	cgcgaacctc	atccagctgt	780
acgatgcctt	cgagctctaa	aacgacattg	tctgtgctat	ggagtattgt	gatggtgggg	840
agctgtttga	ccgcatcatc	gatgagagct	acaatttgac	ggagcttgat	accatcctgt	900
tcatgaagca	gatatgtgag	gggataaggc	acatgcatca	gatgtacatt	ctccacttgg	960
acctgaagcc	tgagaatatc	ctgtgtgtga	atcgggatgc	taagcaaata	aaaattattg	1020
attttggatt	ggccagaaga	tacaaaacca	gagagaagct	gaaggtgaac	tttggaaacc	1080
cagaatttct	cgcccctgaa	gttgtgaact	atgattttgt	ttcatttccc	actgacatgt	1140
ggagtgtggg	ggtcatcgcc	tatatgctac	ttagcggttt	gtcgcctttc	ctgggtgaca	1200
atgatgctga	gacgctgaac	aacatcctgg	cctgcagggtg	ggacttagag	gatgaagaat	1260
ttcaggacat	ctcggaggag	gccaaaggagt	tcattctctaa	gcttctgatt	aaggagaaga	1320
gttggcgaat	aagtgcgaagc	gaagctctca	agcacccttg	gttgtcagac	cacaagctcc	1380
actccagact	caatgcccag	aagaagaaga	atcgtggctc	tgatgcccg	gactttgtga	1440
ccaaatagtc	tacaggaggc	agccatttgg	aaggaaaact	gctgtgggtg	ctgctgcttc	1500
gagaaaaatt	tttgaaaaat	cagcagttct	gatgccttga	cccctgtgat	gacctggtag	1560
ctttagcagg	gggagccctc	gaccctgaat	gtgaacttga	actggagtgc	ctctgtgcgc	1620
tctagaggaa	caccagcgc	tgcggtctgg	tctcagggcg	caaacacatc	cctgcaccgc	1680
gtggtggtga	tgttgggaag	gtgtttccct	gccatctttg	agattttttta	ctttttttaa	1740
aaaa						1744